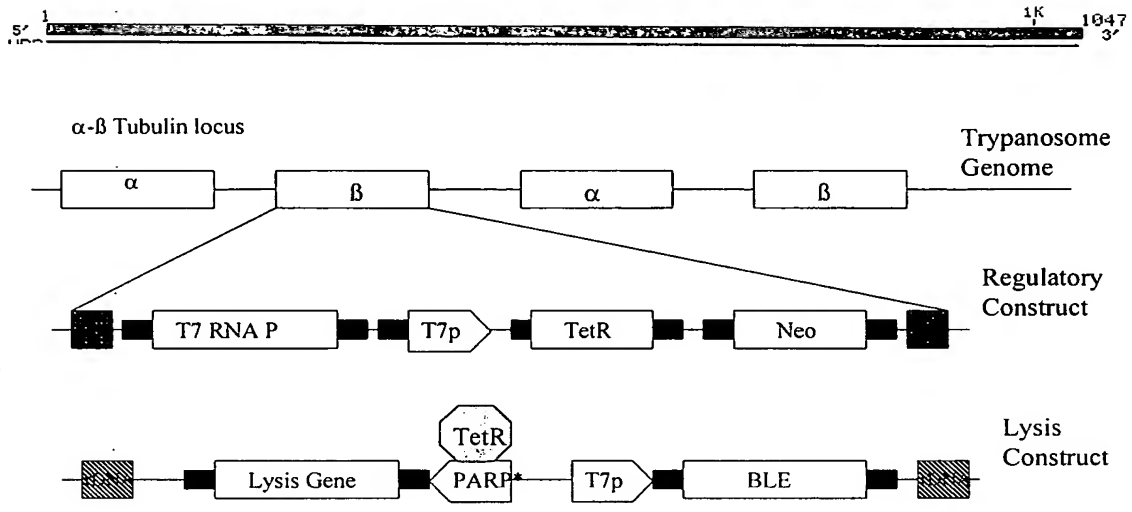
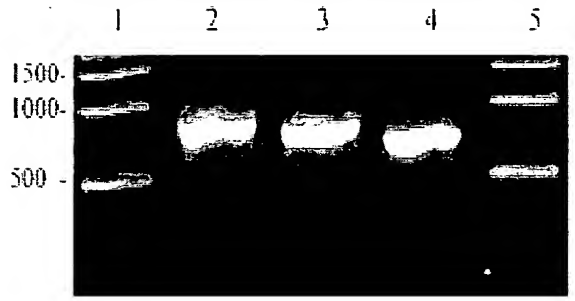


Figure 1

A



B

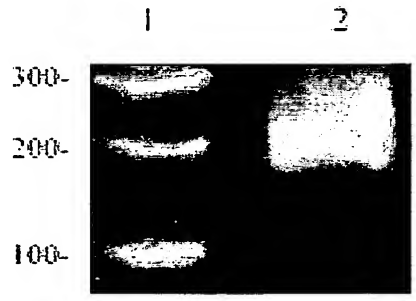


Figure 2

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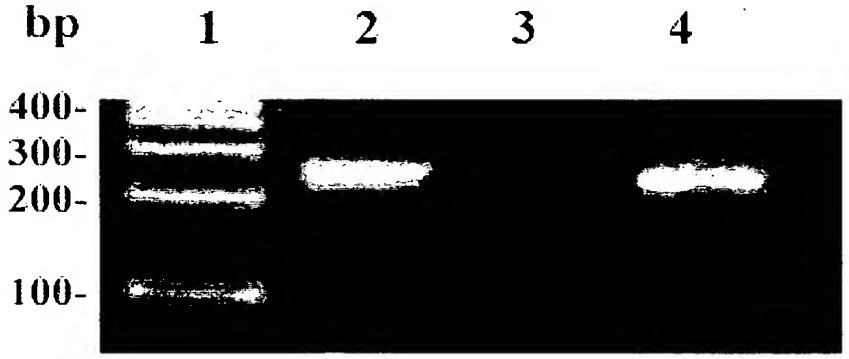


Figure 3

```
promVP4     1 ------------------------------ACCGAAATTAATACGACTCACTATAGGGGAA
promVP3     1 ---------------ATAGCATG-GTACC.............................
                              (KpnI)
promVP2     1 ---------------ATATTAGGCGCGCC.................G...........
                              (AscI)
promVP1     1 AATTATTCGAATTAGCAAGAAGATATTGT.............................
                   (NspV) L  A  R  R  Y  C
promVP4    32 TTGTGAGCGGATAACAATTCCCCGGAGTTAATCCGGGACCTTTAATTCAACCCAACACAA
promVP3    45 ............................................................
promVP2    46 ............................................................
promVP1    61 ............................................................
promVP4    92 TATATTATAGTTAAATAAGAATTATTATCAAATCATTTGTATATTAATTAAAATACTATA
promVP3   105 ............................................................
promVP2   106 ............................................................
promVP1   121 ............................................................
promVP4   152 CTGTAAATTACATTTTATTTACAATCAAAGGAGATAT-AC--------------------
promVP3   165 ....................................T..GCTAGCTACCTACCTTCGAA
(NheI)          (NspV)
promVP2   166 ....................................-..GGCGCCTATAAATCTGCAGA
                                                     (NarI)       (PstI)
promVP1   181 ..................................A-.-GACTAGTAATAAGCGGCCGC
(SpeI)      (NotI)
promVP4       --------
promVP3   225 CTAGTATT
promVP2   225 TTAAT---
promVP1   239 TTTATTTA
```

Figure 4

BEST AVAILABLE COPY

```
native          1 ---GGTGATGTGCAGAATGCTGTCGAAGGGGCTATGGTCAGGGTGGCAGATACAGTGCAA
Recombinant     1 ATG..............T.....................................

native         58 ACTTCAGCCACAAACTCAGAGAGGGTGCCTAACTTGACAGCAGTAGAAACTGGTCACACT
Recombinant    61 ............................................................

native        118 TCGCAGGCAGTACCTGGTGATACCATGCAGACTAGACATGTGATCAACAATCACGTGAGG
Recombinant   121 .......T......................C.............................

native        178 TCAGAATCTACAATTGAGAACTTCCTTGCCAGATCAGCGTGTGTTTTCTACCTAGAGTAC
Recombinant   181 ................................................TG..........

native        238 AAGACAGGGACCAAAGAGGATTCCAATAGCTTCAACAATTGGGTGATTACAACCAGGCGA
Recombinant   241 ..............................G......G.....................

native        298 GTGGCTCAACTACGTAGAAAACTGGAAATGTTTACTTACCTACGGTTTGACATGGAAATC
Recombinant   301 ....G...........T.............................................

native        358 ACCGTGGTCATTACAAGCTCGCAAGATCAGTCTACATCACAAAACCAGAATGCACCAGTG
Recombinant   361 ............................................................

native        418 CTAACACACCAGATAATGTATGTACCACCAGGGGGACCCATACCCGTAAGCGTGGATGAT
Recombinant   421 ..........................................A.................

native        478 TACAGCTGGCAAACATCCACCAACCCCAGTATCTTTTGGACCGAAGGGAACGCTCCGGCA
Recombinant   481 ..............T.............................................

native        538 CGCATGTCAATTCCATTTATTAGCATAGGCAATGCGTATAGTAATTTCTACGATGGGTGG
Recombinant   541 ......................A.....................................

native        598 TCTCACTTCTCCCAGGCTGGCGTGTATGGCTTCACTACTCTGAACAACATGGGTCAATTG
Recombinant   601 ............................................................

native        658 TTCTTCCGGCACGTAAACAAGCCCAACCCAGCCGCTATTACAAGTGTGGCGCGCATTTAC
Recombinant   661 ............................................................

native        718 TTCAAACCGAAACATGTACGCGCTTGGGTGCCTAGACCACCGCGCTTGTGTCCATACATC
Recombinant   721 ............................................................

native        778 AATAGCACGAATGTCAACTTTGAACCCAAGCCAGTGACTGAAGTACGTACCAACATAATA
Recombinant   781 ............................................................

native        838 ACAACG------------------------------------------------------
Recombinant   841 ......ATCATCGCGGCCGCACAGCTGTATACACGTGCAAGCCAGCCAGAACTCGCCCCG

native              ----------------------------------------------
Recombinant   901 GAAGACCCCGAGGATCTCGAGCACCACCATCACCATCACCATCAC
```

Figure 5

```
Native          1 ---TCTCCAACGGTTGAAGAGTGCGGGTACAGTGACAGGGTCAGGTCAATCACACTTGGG
recombinant     1 ATG.............................................................

Native         58 AACTCCACTATTACAACTCAAGAGTGTGCCAATGTGGTGGTGGGGTACGGTGAATGGCCT
recombinant    61 .............................................................

Native        118 GAGTATCTGAGTGATAACGAGGCAACTGCTGAGGACCAACCAACGCAGCCGGACGTGGCC
recombinant   121 .............................................................

Native        178 ACTTGCCGTTTTTACACCCTAGACTCAGTCCAATGGGAGAATGGGTCACCAGGTTGGTGG
recombinant   181 .............................................................

Native        238 TGGAAGTTTCCCGACGCTCTAAGGGATATGGGATTATTTGGCCAAAATATGTACTACCAT
recombinant   241 .............................................................

Native        298 TACTTAGGCAGAGCCGGGTATACCATCCACGTACAATGCAATGCTTCCAAGTTTCATCAA
recombinant   301 .............................................................

Native        358 GGCTGTATCCTGGTAGTGTGTGTCCCTGAGGCGGAGATGGGAAGTGCCCAAACCTCAGGG
recombinant   361 .............................................................

Native        418 GTGGTCAACTACGAACACATTAGTAAGGGTGAGATCGCATCAAGGTTCACTACCACGACA
recombinant   421 .............................................................

Native        478 ACAGCAGAAGACCATGGCGTGCAGGCCGCGGTATGGAATGCTGGTATGGGCGTTGGAGTT
recombinant   481 .............................................................

Native        538 GGGAACTTGACGATCTTCCCGCACCAATGGATCAACCTTCGCACCAACAACAGCGCCACA
recombinant   541 .............................................................

Native        598 ATTGTTATGCCATACGTAAATAGTGTACCAATGGACAATATGTATAGACATCACAACTTT
recombinant   601 .............................................................

Native        658 ACACTAATGATAATACCCTTTGTGCCTCTGGATTTCAGCGCGGGTGCATCCACATACGTG
recombinant   661 .............................................................

Native        718 CCCATAACGGTGACAGTGGCCCCCATGTGTGCCGAGTACAATGGACTACGACTAGCTGGA
recombinant   721 .............................................................

Native        778 CACCAA------
recombinant   781 ......TAGTAG
```

Figure 6

```
native          1 GGTGATGTGCAGAATGCTGTCGAAGGGGCTATGGTCAGGGTGGCAGATACAGTGCAAACT
Recombinant     1 ----.....T.....................................................

native         61 TCAGCCACAAACTCAGAGAGGGTGCCTAACTTGACAGCAGTAGAAACTGGTCACACTTCG
Recombinant    57 ....................-.....................................

native        121 CAGGCAGTACCTGGTGATACCATGCAGACTAGACATGTGATCAACAATCACGTGAGGTCA
Recombinant   116 ....T.......................C.............................

native        181 GAATCTACAATTGAGAACTTCCTTGCCAGATCAGCGTGTGTTTTCTACCTAGAGTACAAG
Recombinant   176 .............................................TG............

native        241 ACAGGGACCAAAGAGGATTCCAATAGCTTCAACAATTGGGTGATTACAACCAGGCGAGTG
Recombinant   236 ............................G......G......................

native        301 GCTCAACTACGTAGAAAACTGGAAATGTTTACTTACCTACGGTTTGACATGGAAATCACC
Recombinant   296 .G...........T.............................................

native        361 GTGGTCATTACAAGCTCGCAAGATCAGTCTACATCACAAAACCAGAATGCACCAGTGCTA
Recombinant   356 .............................................................

native        421 ACACACCAGATAATGTATGTACCACCAGGGGGACCCATACCCGTAAGCGTGGATGATTAC
Recombinant   416 .........................................A...................

native        481 AGCTGGCAAACATCCACCAACCCCAGTATCTTTTGGACCGAAGGGAACGCTCCGGCACGC
Recombinant   476 ............T................................................

native        541 ATGTCAATTCCATTTATTAGCATAGGCAATGCGTATAGTAATTTCTACGATGGGTGGTCT
Recombinant   536 ...................A.........................................

native        601 CACTTCTCCCAGGCTGGCGTGTATGGCTTCACTACTCTGAACAACATGGGTCAATTGTTC
Recombinant   596 .............................................................

native        661 TTCCGGCACGTAAACAAGCCCAACCCAGCCGCTATTACAAGTGTGGCGCGCATTTACTTC
Recombinant   656 ...:.........................................................

native        721 AAACCGAAACATGTACGCGCTTGGGTGCCTAGACCACCGCGCTTGTGTCCATACATCAAT
Recombinant   716 .............................................................

native        781 AGCACGAATGTCAACTTTGAACCCAAGCCAGTGACTGAAGTACGTACCAACATAATAACA
Recombinant   776 .............................................................

native        841 ACG-------------------------------------------------------------
Recombinant   836 ...ATCATCGCGGCCGCACAGCTGTATACACGTGCAAGCCAGCCAGAACTCGCCCCGGAA

native            ------------------------------------------
Recombinant   896 GACCCCGAGGATCTCGAGCACCACCATCACCATCACCATCAC
```

Figure 7

```
Native              1  ATGGGAGCACAGGTATCAACACAGAAGACCGGGGCGCACGAGACTAGCTTGAGCGCTACT
Recombinant         1  ....CGAT.TC.............................................

Native             61  GGCAACTCCATAATACACTACACGAATATTAATTATTACAAAGATGCAGCCTCTAACTCT
Recombinant        61  ........................C.................................

Native            121  GCCAATAGACAAGATTTCACCCAAGACCCTGGTAAGTTTACTGAACCAATGAAAGATGTC
Recombinant       121  ............................C..G..........................

Native                                     181     ATGATAAAAACCCTGCCAGCGCTGAAT------
Recombinant                          181           ............................TCGTAG
```

Figure 8

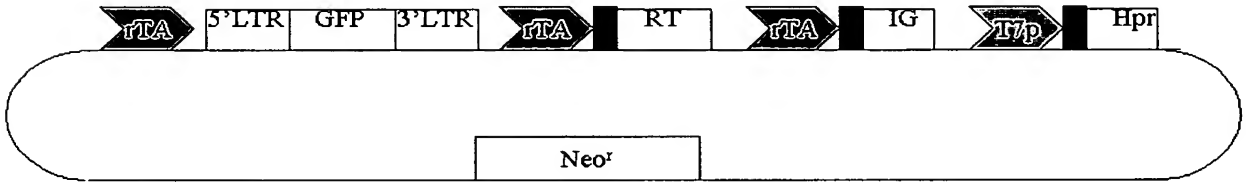


Figure 9

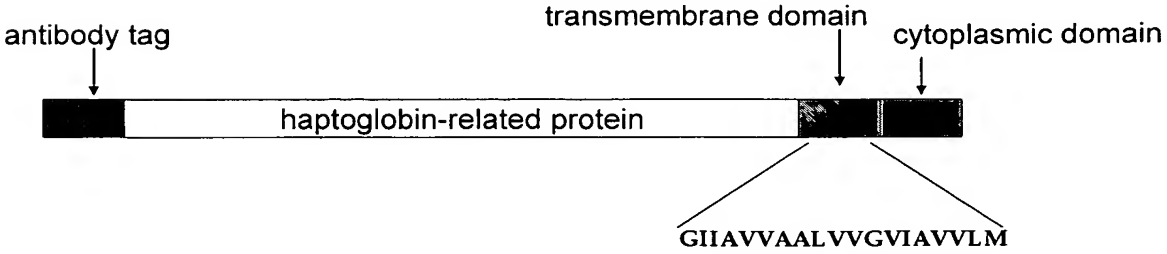
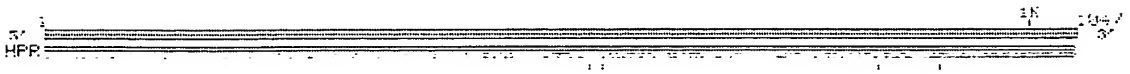


Figure 10



Legend:

CDS = gene = region/SNP

Sequence:

```
1    ATCAGTGACC TGGCAGCTGT CATTTCCGTC CTGCTCTCCG GACCACAGCT TTTTGCACTC TACTCACGCA ATCATGTCAC
       M  S  D  L  C  A  V  I  S  L  L  L  W  C  E  Q  L  F  R  L  Y  S  C  N  D  V  T
81   GAATATTTCA AATGAAAACT TCCCAAAAGC CCGTGAGATT GCACATAACA ATGTGGAAGA CTTGTTTCAC TCCGAATGTA
       D  I  S  N  E  K  F  P  K  P  P  C  I  Q  N  G  Y  V  E  H  I  F  R  Y  Q  C
161  AGAACTACTA CAGACTGCCC ACFCAAGGAG ATGGAGTATA CACCTTAAAT GATAAGAAGC AGTGGATAAA TFAGGCTGTT
       K  N  Y  Y  R  L  R  T  E  G  D  G  V  Y  T  L  N  D  K  K  Q  W  I  N  K  A  V
241  GGAGATAAAC TTCCTGAATG TGFAACAGTA TATGGGAAGC CCAAGAATCC GGCAAACCCA ATGCACCCAA TCCTGAGTGG
       G  D  K  L  P  E  C  E  N  V  C  G  K  P  K  N  P  A  N  P  V  Q  R  I  L  G  G
321  ACACCTGGAT GCCAAAGGCA GCTTTCCCTG GCAAGCTAAG ATGGTTCCCC ACCATAATCT CACCACAGGG GCCACGCTGA
       H  L  D  H  K  G  S  F  P  W  Q  A  K  M  V  S  H  H  N  L  I  T  G  F  I  L
401  TCAATGAACA ATGCCTCCTG ACCACGGCTA AAAATCTCTT CCTCAACCAT TCAGAAATC CAACACCGAA ACACATTCCC
       I  N  E  Q  W  L  L  T  T  A  K  N  L  F  L  N  H  S  E  N  A  T  A  K  D  I  R
481  CCTACTTAAA CAGTCAATGT GGGGAAAAAG CAGCTTGTAG TGATTAGAGT GGTGGTTCAA CAGCCTAACT ACCACCAAGT
       T  E  -  Q  C  K  W  K  K  L  V  I  L  L  K  V  V  L  H  P  N  Y  H  W  V
561  AGATATTGGG CTCATCAAAC TCAAACAGAA GGTGCTTGTT AATGAGAGAA TGATGCCCAT CTGCCTACCT TCAAAGAATT
       D  I  G  L  I  K  L  K  Q  K  V  L  V  N  E  R  V  M  P  I  C  L  P  S  K  E  L
641  ATCCAGAAGT AGGCCGTCTG CCTTACGTCT CTGGCTGCCC ACAAACTGAC AACTTTAAAC TTACTCACCA TCTCAACTAT
       Y  A  E  V  G  R  V  S  Y  V  S  G  W  C  Q  S  D  N  F  K  L  T  D  H  L  K  Y
721  GTGATGCTAC CTGTGAGTGA GGGATGAGAT TGGATAAGAA ATTCTAAAGA GAAAACATGA GCCAAATGAA AGAAACAAAA
       V  M  L  P  V  A  D  E  Y  D  C  T  T  H  Y  E  G  S  T  C  P  K  W  K  A  P  K
801  GAGCCCTGTA GGGCTGCAGC CCFTACTGAA CGAACACACC TTCTGTGTCC GCATGTCTAA GTACCAGGAA GFCACCTGCT
       S  P  V  G  V  Q  P  I  L  N  E  H  T  F  C  V  G  M  S  K  Y  Q  E  I  T  C
881  ATGGCGATGC GGGCAGTGCC TTTGCCGTTC ACGACCTGGA GCAGGACACC TGGTACGCGC CTGGGATCCT AFGCTTTGAT
       Y  G  D  A  N  S  A  F  A  V  H  D  L  E  E  D  T  W  Y  A  A  G  I  L  S  F  D
961  AAGAGCTGTG CTGTGGCTGA GTATCGTGTG TATGTGAACG TGACTTCCAT CCAGGACTGC GTTCAGAAGA CCATAGCTGA
       K  S  C  A  V  A  E  Y  G  V  Y  V  K  V  T  S  I  Q  D  W  V  Q  K  T  I  A  E
1041 CAACTAA
```

Figure 11